(LPS), which are part of the 'O' antigen. Over 100 types of 'O' groups have been detected in ETEC strains in combination with different flagellar (H) antigens, that together make the serotype (O:H) of the bacteria. Although extensive efforts have been made to determine the prevalence of the toxins and colonization factors in ETEC strains isolated in different regions of the world, relatively little is known about the serotype of the bacteria circulating in different countries, especially those that are prevalent at this time.

Recent epidemiological studies have shown that ETEC strains from different regions differ in their phenotypic characteristics. These findings are important to determine which vaccines would be suitable for use in one region but not in another as a measure of protection against ETEC infections. ETEC isolated from two geographically different locations, Mexico and Bangladesh, have been characterized for their 'O' and 'H' antigens as well as for their enterotoxin types and colonization factor production. Overall a variety of ETEC phenotypes were found to be present in both settings. Twelve serotypes were common in both settings. A few serogroups were only present in isolates from Bangladesh (O20, O115, O126, O128, O114), while others were present only in strains isolated in Mexico (O103, O170, O22). The predominant colonization factors in both settings were CFA/I, CS5+CS6, CS6 as well as CS1+CS2/CS3. Colonization factors were produced by strains belonging to a few 'O' serogroups, CFA/I (O126 and O128), CS5+CS6 (O115 and O167), CS6 (O169), CS1+CS2/CS3 (O6). Based on these results, formulation of an effective multivalent ETEC vaccine will have to include not only the major colonization factors and LT toxoid but also the LPS of important serogroups. An inactivated killed ETEC vaccine that has undergone extensive testing includes strains of serogroups O6, O25, O78 and O167. Based on the present data this vaccine would in addition need the incorporation of strains belonging to serogroups O115 and O126 to be more effective in the protection against the most common cause of bacterial diarrhea in early childhood and the second most predominant cause of diarrhea in adults in endemic countries, including tourists travelling to these areas.

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Typhoid Vaccines as Routine Public Health Tools for Developing Countries: An Idea Whose Time Has Come

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Despite the availability of two internationally licensed, newer generation typhoid vaccines that are safe and effective and despite an annual global typhoid mortality burden estimated at over 200,000 deaths, typhoid vaccines are not routinely used as public health interventions in developing countries with high typhoid burdens. Although there are multiple reasons for the failure to introduce these vaccines into public health programs for the poor, a gap in evidence to inform vaccine policy is a major factor. To address this gap in evidence, the International Vaccine Institute, of research, called the Diseases of the Most Impoverished (DOMI) Program, to inform policy about typhoid vaccine introduction in Asia. This research program, which has been undertaken in Bangladesh, China, India, Indonesia, Pakistan, and Vietnam, has demonstrated the burden of typhoid fever to be high, but geographically heterogeneous. The research has also demonstrated a high financial cost associated with typhoid fever, and a modest cost of purchasing and delivering one of the two currently available, internationally licensed typhoid vaccines (Vi polysaccharide). Demonstration projects with Vi vaccine have shown that the vaccine is feasibly delivered in mass immunization campaigns in both school and community settings, and when delivered in these campaigns the vaccine confers both direct and herd protection. As well, there is a high population demand for a vaccine with the cost and characteristics of Vi polysaccharide, and even a willingness on the part of developing country populations to pay for this vaccine, particularly for vaccination of children. In aggregate, these findings have helped to motivate a recently published, strengthened WHO recommendation for routine typhoid vaccination in settings with high typhoid disease burdens.

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5.003

The New Emerging Strain of Cholera: One Step Ahead of Genomics

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A remarkable event in recent years has been the emergence of strains of Vibrio cholerae O1 that possess traits of both the classical and El Tor biotypes. These strains were first encountered from sporadic cases of cholera isolated from 1992 onwards in Matlab, Bangladesh. Phenotypic and genotypic traits failed to categorize these strains into classical or El Tor biotype and were designated as the Matlab variants. The Matlab variants assumed greater significance when strains of V. cholerae O1 isolated from Beira, Mozambique in 2005 displayed typical traits of the El Tor biotype but carried the classical CTX prophage. A more recent analysis of V. cholerae O1 strains isolated in Bangladesh during the past four and a half decades revealed that from 2001 onwards all strains associated with cholera belonged to the El Tor biotype but produced classical cholera toxin (CT) which was different from the prototype El Tor biotype that produced El Tor CT. This new variant of the El Tor biotype is now dominant in several other countries. At this time, it is not certain whether the change in CT subtype in the El Tor strains will enhance their epidemic potential. Given that there are differences between the classical and El Tor biotypes, the selection of the El Tor biotype which produces classical CT would seem to indicate an evolutionary optimization of the El Tor biotype and represents a new more efficient emerging form of the El Tor biotype. Under the cholera surveillance program of the International Centre for Diarrheal Disease Research in Bangladesh, an increasing trend in the number